

AMENDMENTS

In the Specification:

Please amend the paragraph starting on page 8, at line 10 and continuing on page 9, thru line 4 as follows:

Still another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2-containing molecule comprising the amino acid sequence ~~ALNPPNYLISKDVTG~~ ALNPDNYLISKDVTG <400>1 or ALNPDNYLISKDVTGATKVKY <400>8 or an amino acid sequence having at least 40% similarity to <400>1 or <400>8 or at least about 20% identity after optimum alignment with same sequence or an amino acid sequence encoded by the nucleotide sequence <400>7 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridizing thereto under low stringency conditions and an HA2-binding motif comprising and including propionic acid groups or anionic or salt forms thereof such as but not limited to the region defined by substructure (Ic) in Formula (I) on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

Please amend the paragraph starting on page 24, line 13 as follows:

Accordingly, another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2-containing molecule comprising the amino acid sequence ~~ALNPPNYLISKDVTG~~ ALNPDNYLISKDVTG <400>1 or ALNPDNYLISKDVTGATKVKY <400>8 or an amino acid sequence having at least 40% similarity to <400>1 or <400>8 or at least about 20% identity after

optimum alignment with same sequence or an amino acid sequence encoded by the nucleotide sequence <400>7 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridizing thereto under low stringency conditions and an HA2-binding motif comprising and including propionic acid groups or anionic or salt forms thereof such as but not limited to the region defined by substructure (Ic) on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.